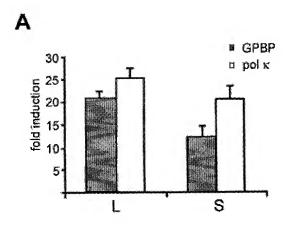
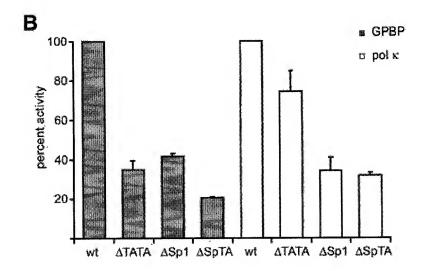
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Apai CREARICGECCTRESSASSEDIFICEDTERSCTTCAGORIANICTCTETCAGTTCTGGCCCCCANSECCTRONGETTCTTCTANAACA CTGTTCGGCCCCACCCTTTCGTCCGCCCGAGAGAGAGAGA	450
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\$P CCCABATTGCAGEA-AGCTREATT CTTA-CCGCCCTTTCTTTTTTTCTCTCTCTTCTTCTTCTTCTTCT	350
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CHCDOMEGACTCABOGGCCOMPTTTCCTTTCCTTTCTTTTCCTTTCTTTCCTTCCTTCCT	833

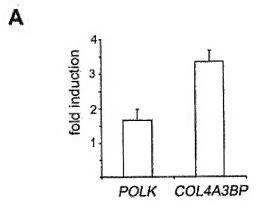


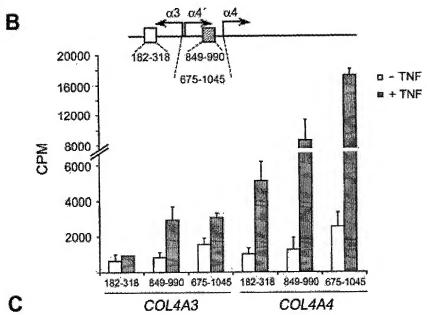


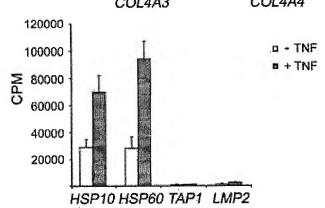
	COL4A3BP	POLK 🗆	Alignment map*
COL4A1-A2 (α ₁ α ₂) GenBank no M36963	Region aligned 469-608 Q =620; $E(Q)$ =591.4±17.1 z =1.6725, P =0.00472	Region aligned 583-722 Q=580; E(Q)=571±19 z=0.4737, P=0.3179	$\alpha 1 \alpha 2$
COL4A3-A4 (α ₃ α ₄) GenBank no. AF218541	Region aligned 849-990 Q=674; E(Q)=568.7±17.5 z=6.0171, P<0.0001	Region aligned 182-318 Q =641; $E(Q)$ =557.5±18.4 z =4.5380, P <0.0001	α3 α4′ α4
$COL4A5-A6$ $(\alpha_5\alpha_6)$ GenBank no D28116	Region aligned 1714-1853 Q =570; $E(Q)$ =524.2±18.4 z =2.4891, P =0.0064	Region aligned 440-579 Q =570; $E(Q)$ =527.4±17.3 z =2.4624, P =0.0069	α5 α6΄ α6

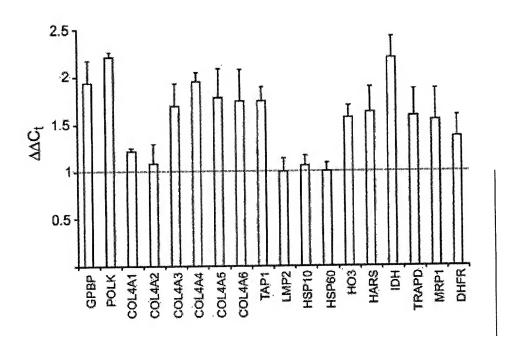
Q is a measure of the quality of the alignment. E(Q) is the Q value expected by chance. z-score for Q. This score is normally distributed with mean zero and variance 1. P is the probability of observing Q just by chance. *In the drawing (\vdash ~ 0.5 kb) are indicated the statistically significant alignments (P values in boldface).

		COL4A3BP	$POLK \square$	Alignment map*
_	LMP2-TAP1 GenBank no. X66401	Region aligned 24579-24718 Q =610; $E(Q)$ =549.9±16.9 z =3.5562, P =0.0002	Region aligned 27355-27494 Q =620; $E(Q)$ =582.8±18.6 z =2, P =0.0228	LMP2 TAP1
	MRP1-DHFR GenBank no. K01612	Region aligned 849-991 Q =581; $E(Q)$ =557.7 \pm 20.8 z =1.1202, P =0.1313	Region aligned 704-843 Q =640; $E(Q)$ =553.4±18.1 z =4.7845, P <0.0001	DHFR DHFR' MRP1
	GPAT-AIRC GenBank no U00239	Region aligned 632-769 Q =554; $E(Q)$ =573.4±20.4 z =-0.9510, P =0.8292	Region aligned 561-705 Q =565; $E(Q)$ =549.4±18.4 z =0.8478, P =0.1983	
	HO3-HRS GenBank no. M96646	Region aligned 313-452 Q=600; E(Q)=531±17.5 z=3.9429, P<0.0001	Region aligned 214-353 Q =560; $E(Q)$ =557.1±16.2 z =0.1790, P =0.4290	HRS HRS'
	HSP10-HSP60 GenBank no. AJ250915	Region aligned 3451-3590 Q=600; E(Q)=546.7±16.7 z=3.1916, P=0.0007	Region aligned 3684-3821 Q =594; $E(Q)$ =542.6±17.1 z =3.0058, P =0.0013	HSP10 HSP60
	IDHG-TRAPD GenBank no. Z68129	Region aligned 16283-16422 Q =622; $E(Q)$ =594.8±16.5 z =2.7394, P =0.0031	Region aligned 14190-14329 Q =610; $E(Q)$ =601.9±15.5 z =0.5226, P =0.3006	









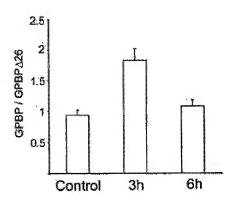


FIGURE 8 B6-bcl-2-Tg(+) NZW GN: GPBP / GPBPΔ26: 0.6 - 0.9 1.6 - 3.0 B Nº 4 Nº 1 αCD4 GN: 1.9 GPBP/GPBPA26: 2.3 Nº 10 Nº 14 αCD4/Ø + 4.2 GN: 4.7 GPBP / GPBPΔ26: Nº 2 Nº 3 α CD4 / α TNF GN: ++ 2,3 2.5 GPBP / GPBPA26: 2500 2000 00 1500 1000 500 αCD4/Ø αCD4 / αTNF F1 Tg(-)

F1 Tg(+)

